

## REPLACEMENT SHEET

10%  
45

Fig. 10

human	: G D V E K G K K I F I M K C S Q C H T V E G G K H K T G P N L H G L F G R K	SEQ ID NO: 1
bacterium	: E G D A A A G E R E V S K K K C L A C H T F D Q G G A N K V G P N P N L F G V F	SEQ ID NO: 2

homology: 47%

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45

Fig. 11

Rat : MSLAILRVIRLVRVFRIFKLSRHSKGLQILGRTLKASMRELGLLFIGVV

leucinzip. L(6)L(6)L(6)L(6)L

SEQ ID NO: 3

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45

Fig. 12

SEQ ID NO: 1  
human : G O V E K G K K I F I M K C S O C H T V E K G G K H K T G P N I H G L F G R K ...  
bacterium : E G D A A G E K V S K K C L A C H T F D Q G G A N K V G P N P N L F G V F ...  
SEQ ID NO: 2

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Fig. 23 A

1	TEEQIAEFKE	AFSLFDKDGD
21	GTITTKELGT	VMRSLGQNPT
41	EAELQDMINE	VDADGNGTID
61	FPEFLTMMAR	KMKDTDSEEE
81	IREAFRVFDK	DGNGYISAEE
101	LRHVMTNLGE	KLTDEEVDEM
121	IREANIDGDG	QVNYEEFVQM
141	MTA	

AMINO ACID SEQUENCE OF CALMODULIN SEQ ID NO: 4  
(EXCERPT FROM PDB)

Fig. 23 B

1	AMDQQAEARA	FLSEEMIAEF
21	KAAFDMFDAD	GGGDISTKEL
41	GTVMRMLGQN	PTKEELDAII
61	EEVDEDGSGT	IDFEELFLVM
81	VRQMKEDAKG	KSEEEELADCF
101	RIFDKNADGF	IDIEELGEIL
121	RATGEHVTEE	DIEDLMKDSD
141	KNNDGRIDFD	EFLKMMEGVQ
161		

AMINO ACID SEQUENCE OF TROPONIN C SEQ ID NO: 5  
(EXCERPT FROM PDB)

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Fig. 25

Probe site = 81-108 in Calmodulin

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	SEQ ID NO: 6
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	< target >
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe >
III	II2	II3	II4	II5	II6	II7	II8	II9	II9	II0	II1	II2	II3	SEQ ID NO: 7	
I	D	I	E	E	L	G	E	I	L	R	A	T	< target >	SEQ ID NO: 6	
I	S	A	A	E	L	R	H	V	M	T	N	L	< probe >	SEQ ID NO: 7	

rmsd = 0.567034

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45

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Fig. 26

Probe site = 81-108 and 117-143 in Calmodulin

96 97 98 99 100 101 102 103 104 105 106 107 108 109 110  
 L A D C F R I F D K N A D G F < target >  
 I R E A F R V F D K D G N G Y < probe >  
 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125  
 I D I E E L G E I L R A T < target > SEQ ID NO: 6  
 I S A A E L R H V M T N L < probe > SEQ ID NO: 7  
 132 133 134 135 136 137 138 139 140 141 142 143 144 145  
 I E D L M K D S D K N N D G < target >  
 V D E M I R E A N I D G D G < probe >  
 146 147 148 149 150 151 152 153 154 155 156 157 158 159  
 R I D F D E F L K M M E G < target > SEQ ID NO: 8  
 Q V N Y E E F V Q M M T A < probe > SEQ ID NO: 9

rmsd = 0.823665

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Fig. 29

ATP/GTP binding site

Probe = (elongation factor)

7 8 9 10 11 12 13 14  
G H V D H G K T < probe >

SEQ ID NO: 10

8 9 10 11 12 13 14 15  
G A P G S G K < target >  
G H V D H G K T < probe >  
rmsd=0.648732 adenylate kinase

unit - A

10 11 12 13 14 15 16 17  
G A G G V G K S < target >  
G H V D H G K T < probe >  
rmsd=0.421770 ras protein

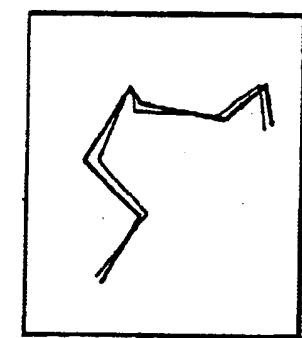
REPLACEMENT SHEET 1



Fig. 30

PROSITE

ATP/GTP binding site  
(P-loop)  
[AG]-X(4)-G-K-[ST]



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Fig. 38 A

1	I V G G Y T C C A N	T V P Y Q V S L N S
21	G Y H F C G G S L I	N S Q W V V S A A H
41	C Y K S G I Q V R L	G E D N I N V V E G
61	N E Q F I S A S K S	I V H P S Y N S N T
81	L N N D I M L I K L	K S A A S L N S R V
101	A S I S L P T S C A	S A G T Q C L I S G
121	W G N T K S S G T S	Y P D V L K C L K A
141	P I L S D S S C K S	A Y P G Q I T S N M
161	F C A G Y L E G G K	D S C Q G D S G G P
181	V V C S G K L Q G I	V S W G S G C A Q K
201	N K P G V Y T K V C	N Y V S W I K Q T I
221	A S N	SEQ ID NO: 14

AMINO ACID SEQUENCE OF TRYPSIN (EXCERPT FROM PDB)

Fig. 38 B

1	V V G G T E A Q R N	S W P S Q I S L Q Y
21	R S G S S W A H T C	G G T L I R Q N . W V
41	M T A A H C V D R E	L T F R V V V G E H
61	N L N Q N N G T E Q	Y V G V Q K I V V
81	P Y W N T D D V A A	G Y D I A L L R L A
101	Q S V T L N S Y V Q	L G V L P R A G T I
121	L A N S P C Y I T T	G W G L T R T N G Q
141	L A Q T L Q Q A Y L	P T V D Y A I C S S
161	S S Y W G S T V K N	S M V C A G G D G V
181	R S G C Q G D S G G	P L H C L V N G Q Y
201	A V H G V T S F V S	R L G C N V T R K P
221	T V F T R V S A Y I	S W I N N V I A S N

SEQ ID NO: 15

AMINO ACID SEQUENCE OF ELASTASE (EXCERPT FROM PDB)

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Fig. 39 A

Key site number 36 - 41 in Trypsin

41 42 43 44 45 46  
M T A A H C < target > SEQ ID NO: 16  
V S A A H C < probe > SEQ ID NO: 17

$d = 12.070038$  [A]

r.m.s.d. = 0.061077 [A]

The number of atoms in a probe = 6

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF HISTIDINE ACTIVE SITES

Fig. 39 B

Key site number 175 - 179 in Trypsin

186 187 188 189 190  
G D S G G < target > SEQ ID NO: 18  
G D S G G < probe > SEQ ID NO: 19

$d = 8.922721$  [A]

r.m.s.d. = 0.092879 [A]

The number of atoms in a probe = 5

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

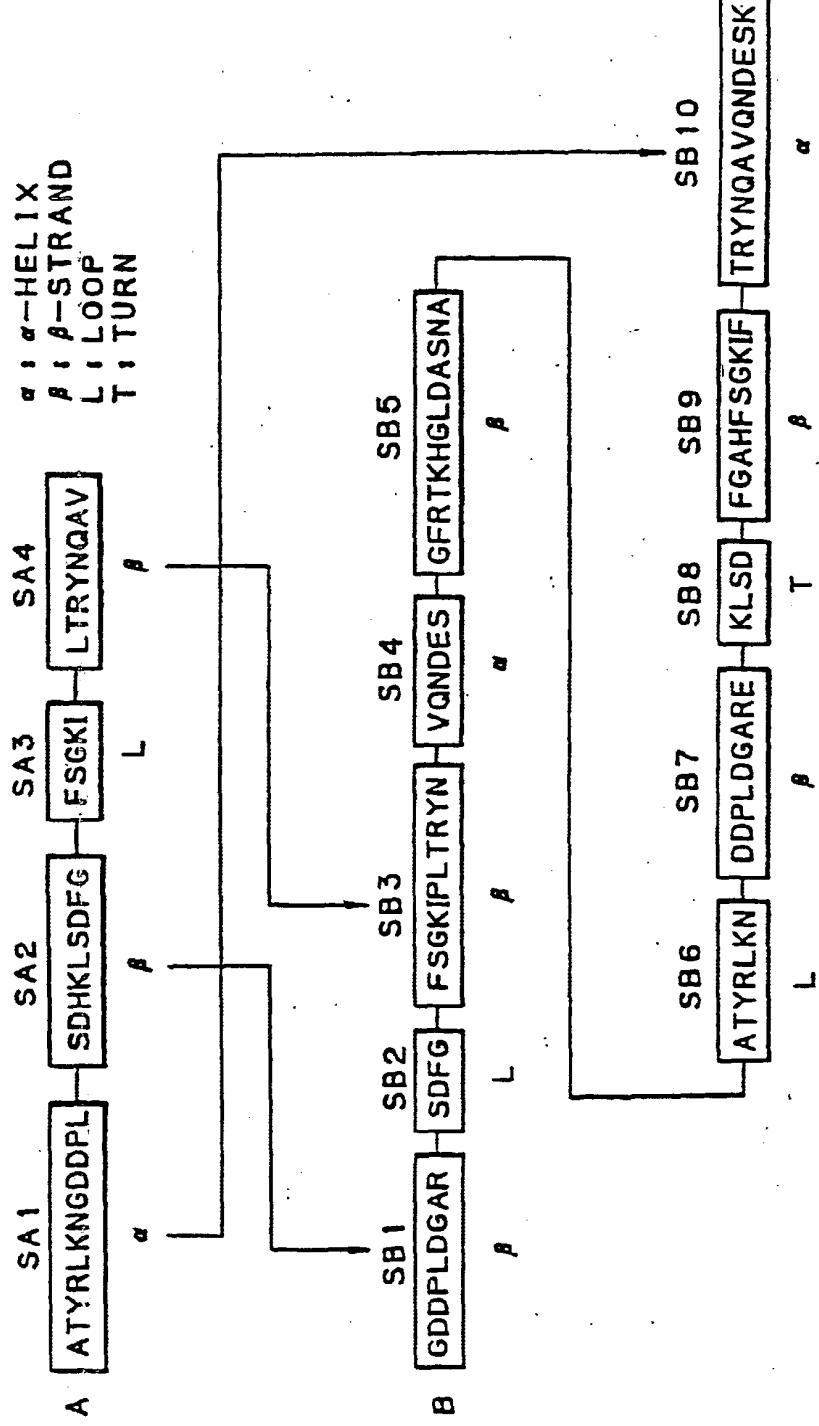
RETRIEVED RESULTS OF SERINE ACTIVE SITES

REPLACEMENT SHEET



44  
45

Fig. 46



SEQ ID NO: 20